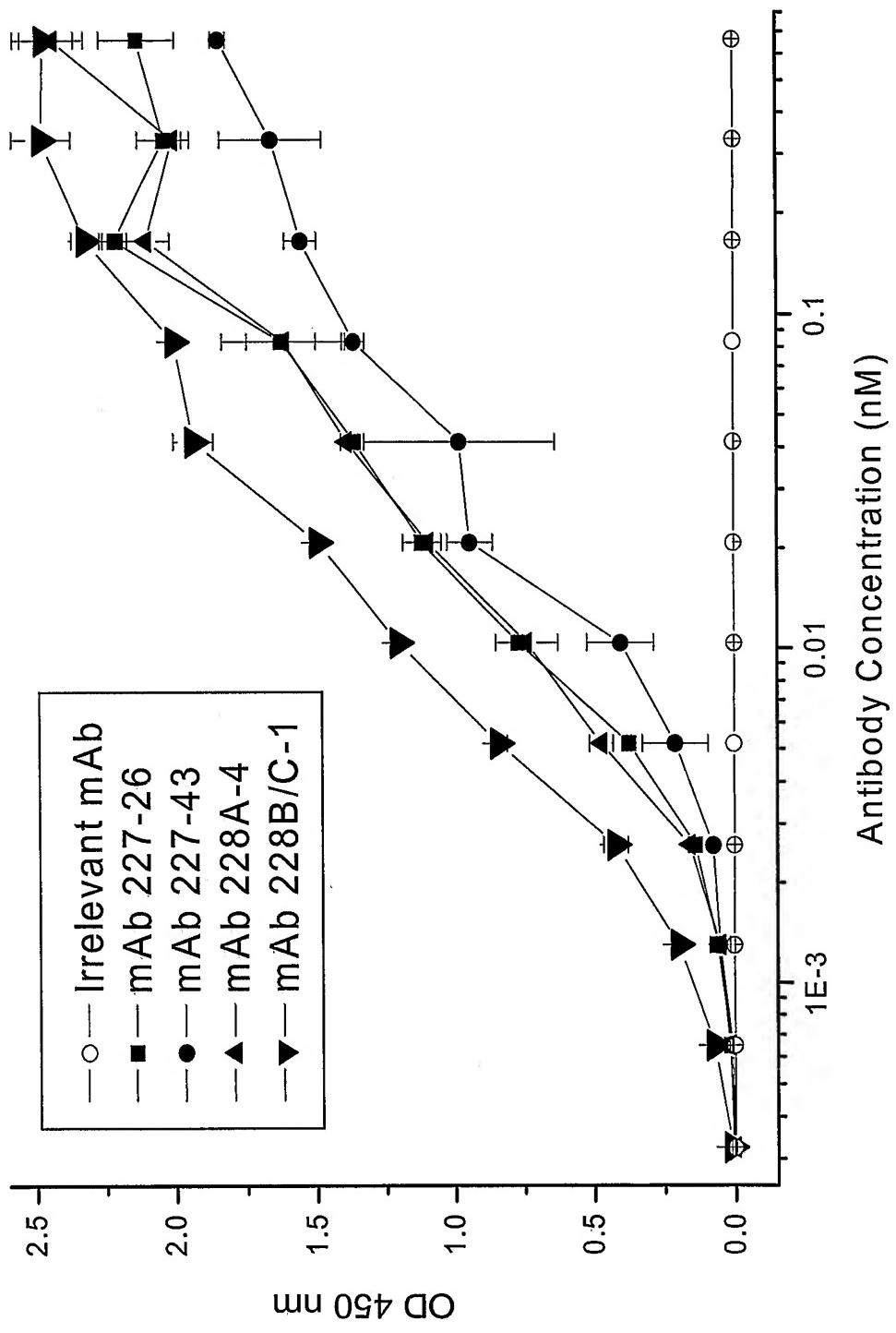
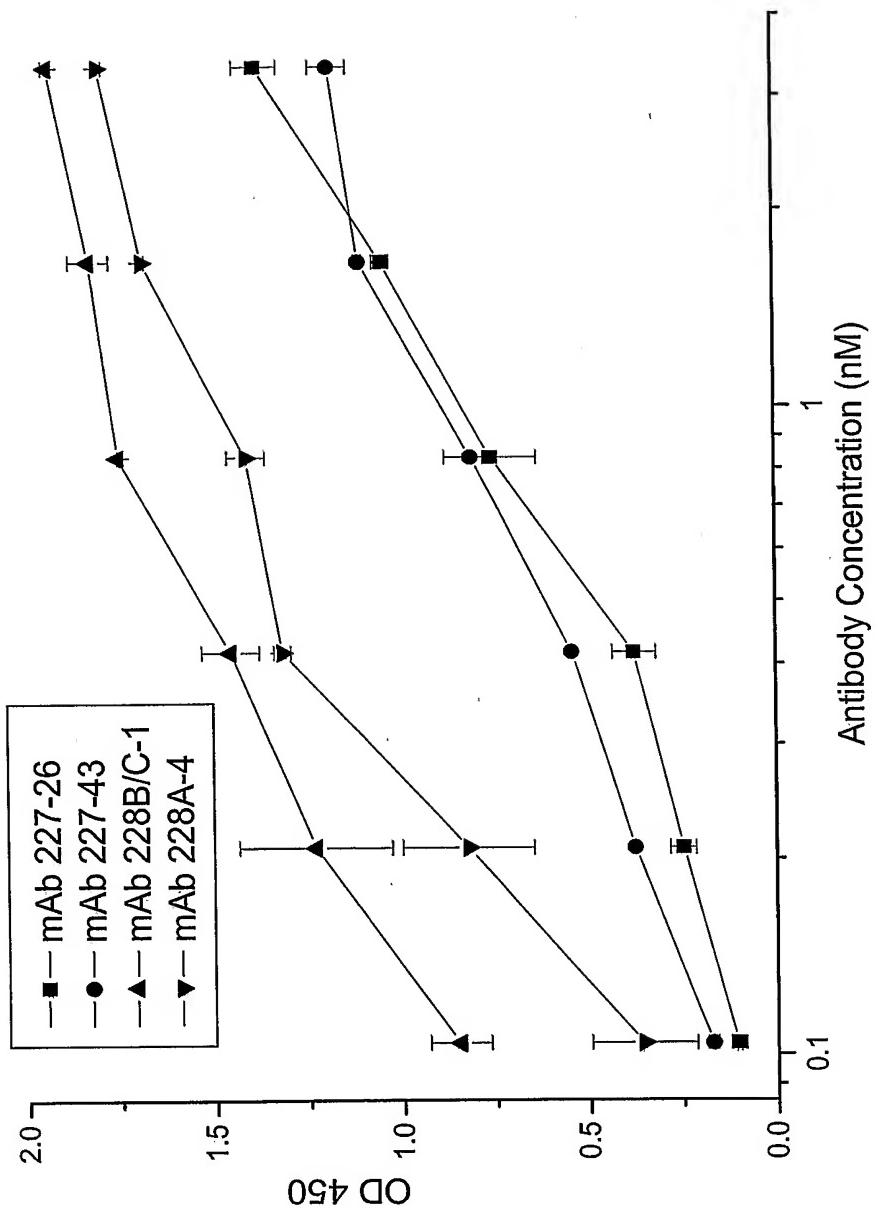


**Fig. 1 Binding of anti-IL13 mAbs to human IL-13 in ELISA**



**Fig. 2 Binding of anti-IL13 mAbs to MT-IL13/Fc**



**Fig. 3 Anti-IL13 mAb JES10-5A2 does not compete with the binding of mAb 228B/C-1-HRP to Human IL-13 in ELISA**

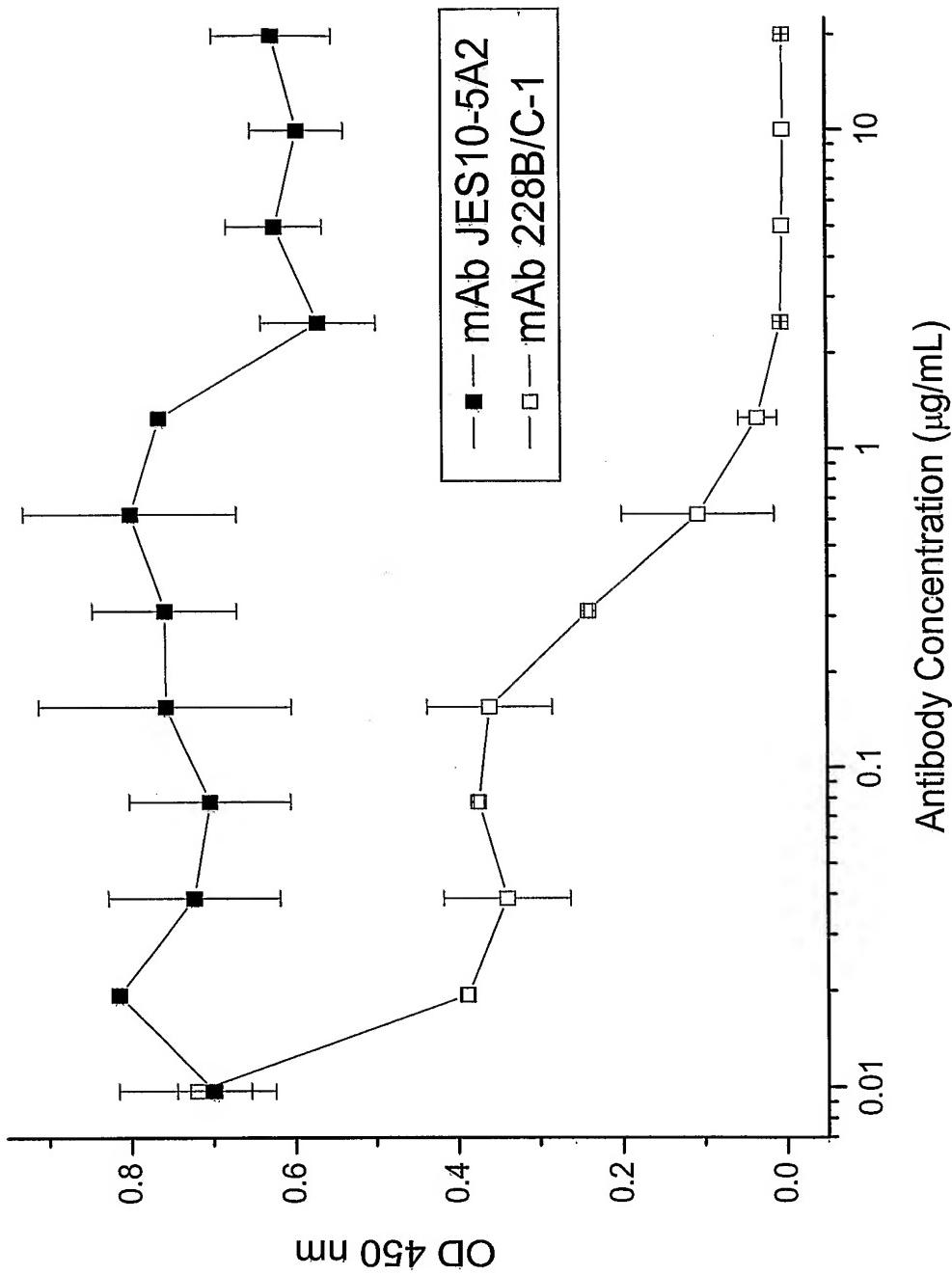
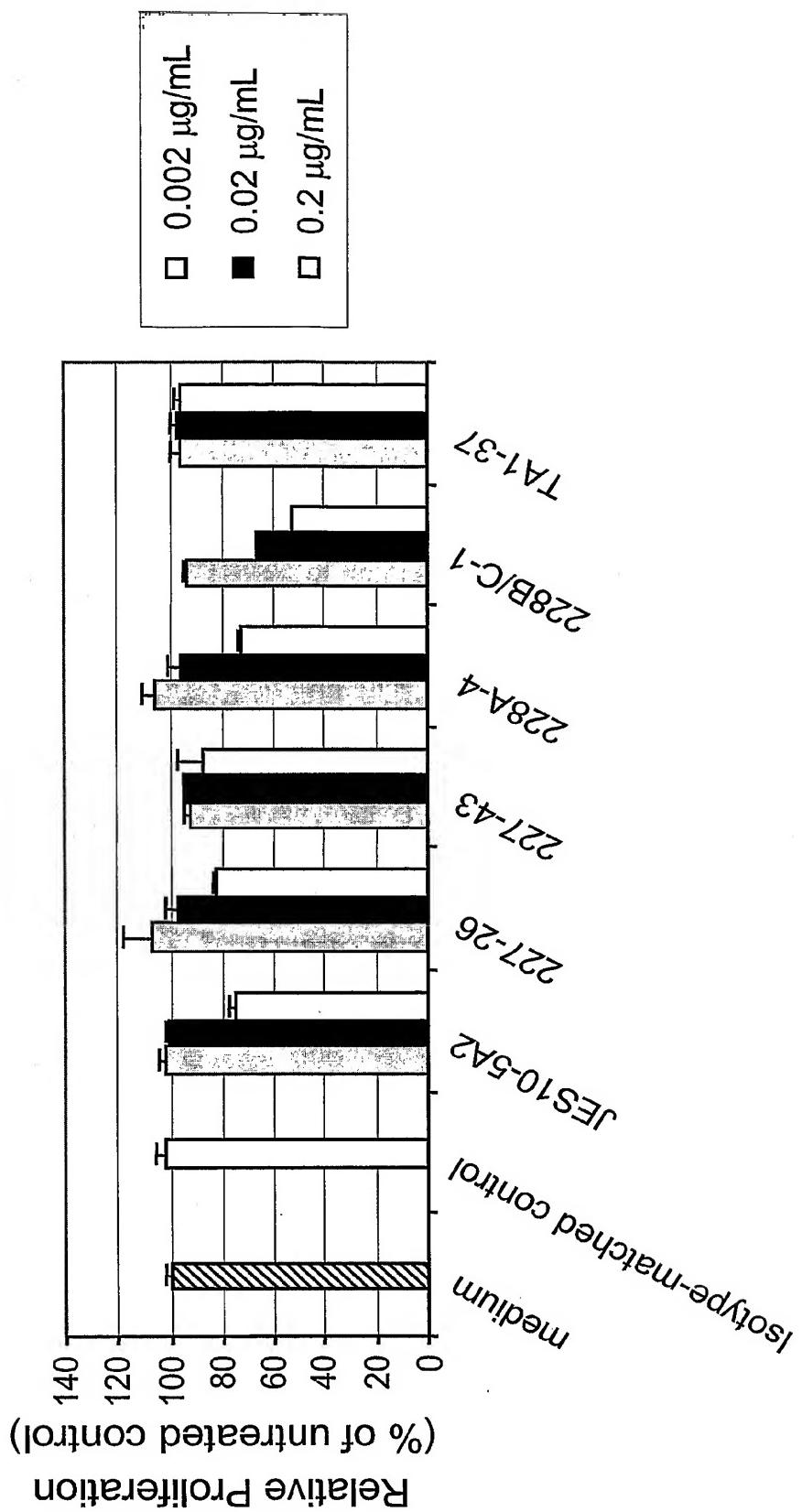
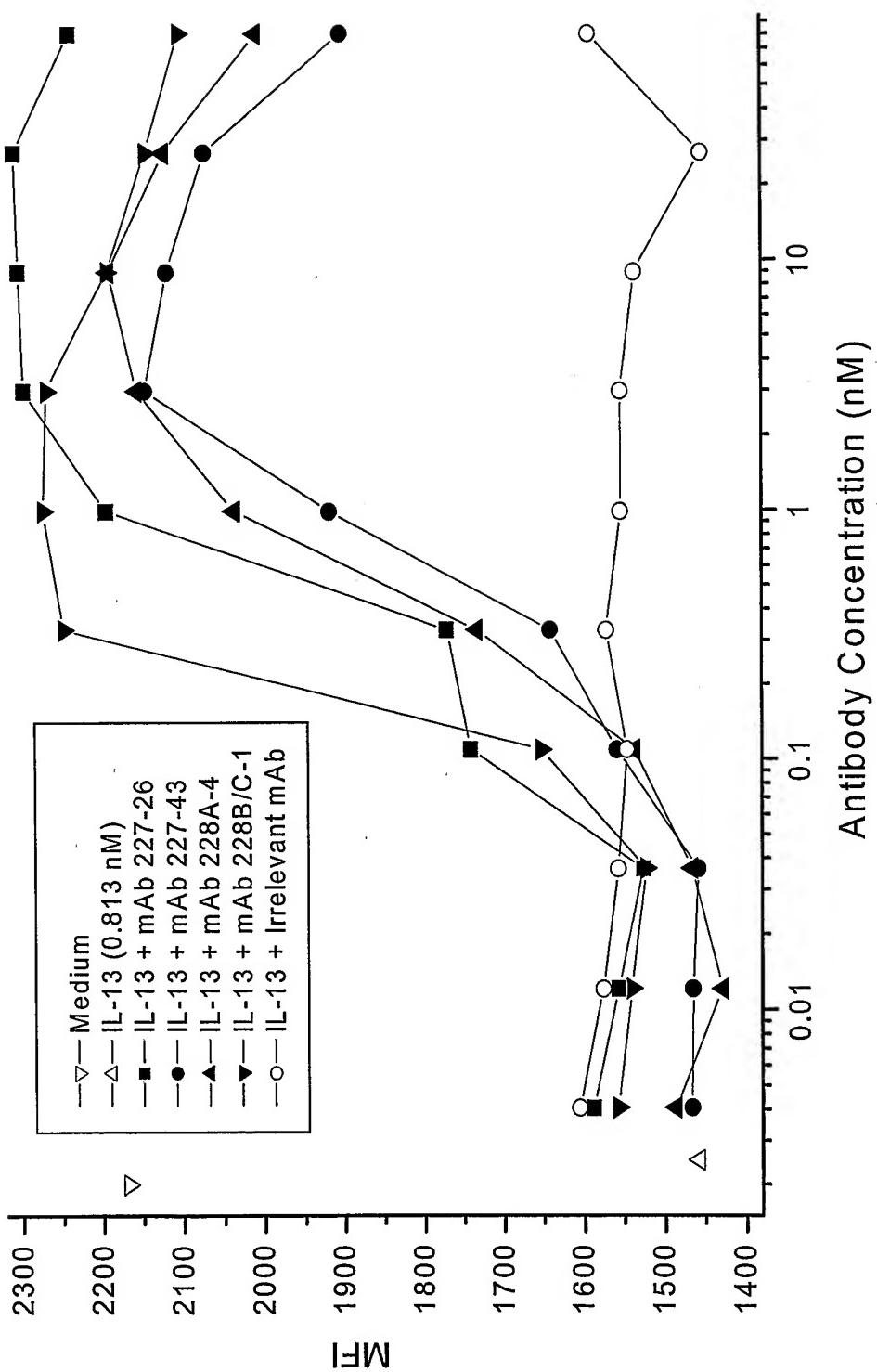


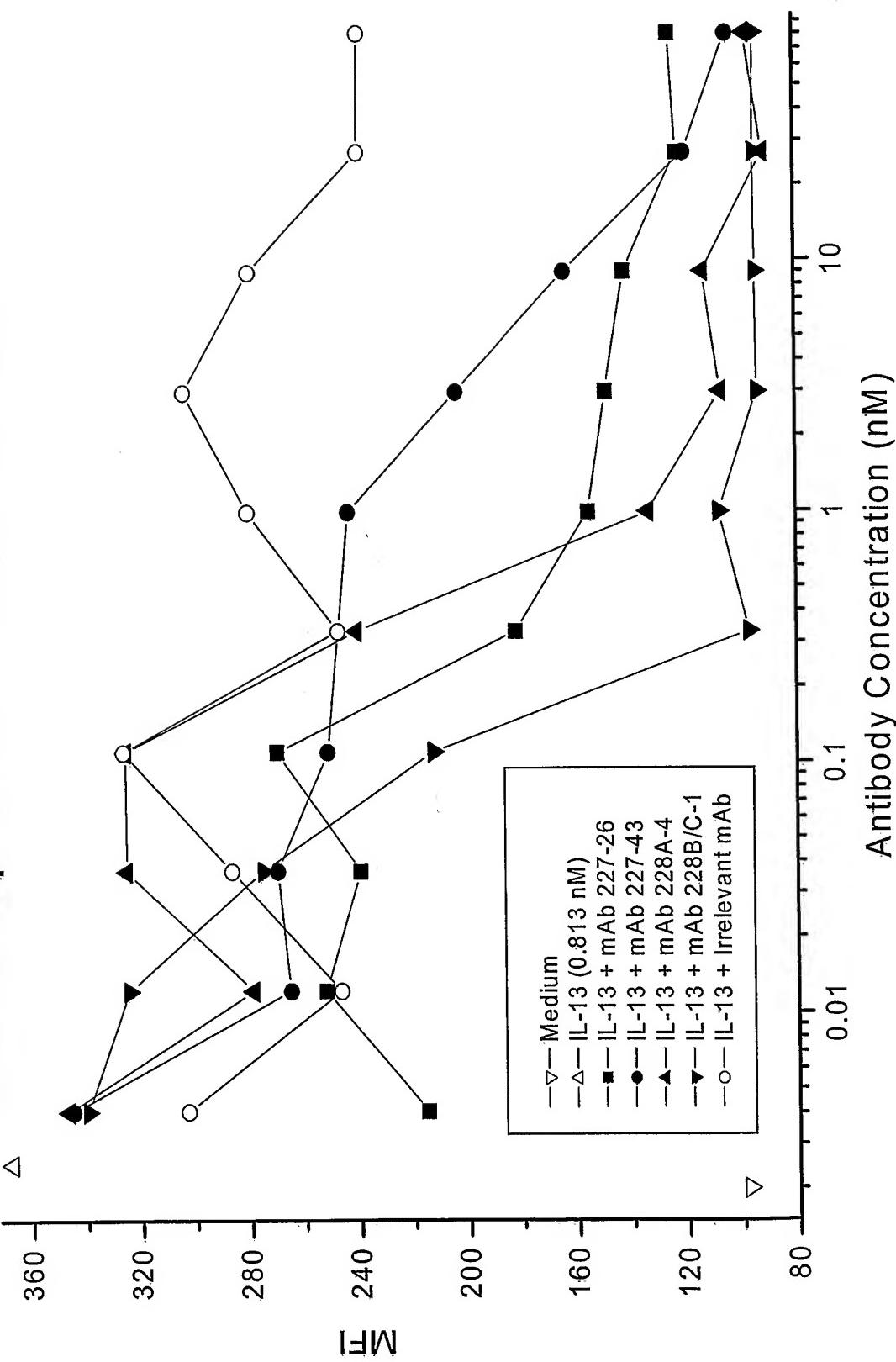
Fig. 4 Effect of anti-IL13 mAbs on the proliferation of L-1236 cells



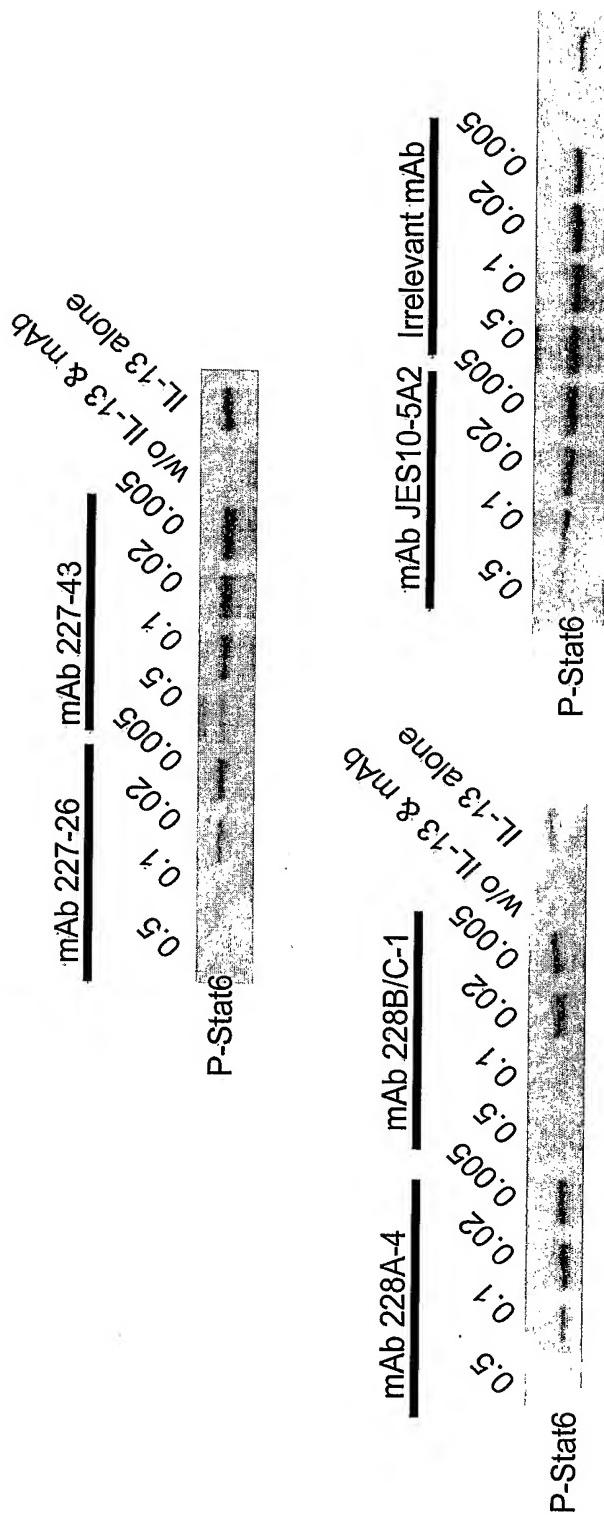
**Fig. 5** Effect of anti-IL13 mAbs on IL13-induced suppression of CD14 expression in human monocytes



**Fig. 6** Effect of anti-IL13 mAbs on IL13-induced upregulation of CD23 expression in human monocytes



**Fig. 7 Anti-IL 13 mAbs Inhibit IL 13-Induced Stat6 Phosphorylation in THP-1 Cells**



**FIGURE 8**

228B/C-1 Antibody  
Heavy Chain (VH)

1	Q V Q L Q E S S G P G L V A P S Q S S L S I T C T V S G F S L N A Y S V N W V
20	20
40	R Q P P G K G L E W L G M I W G D G K I V Y N S A L K S R L N I S K D S S
50	50 52a 53
60	60
70	65 70
80	80 82
90	90
95	95
100	b c d e f 101
K S Q V F L K M S S I Q S D D T A R Y Y C A G D G Y Y P Y A M D N W G H G T	100

Light Chain (VK)

N I V L Q S P A S L A V S L G Q R A T I S C R A S S K S V D S Y G N S F M H W  
Y Q Q K P G Q P P K L L I Y L A S N L E S G V P A R F S G S G S R T D F T L T I  
D P V E A D D A S S Y Y C Q Q N N D P R T F G G G T K L E I K R A 113  
80 90 100 70  
40 50 60  
10 20 30

Underlined: Kabat CDR. Bold/italic: Chothia CDR1.

**FIGURE 9**  
**228A-4 Antibody**  
**Heavy Chain (VH)**

<p><b>Light Chain (VK)</b></p> <pre> 1 N I V L T Q S P T S L A V S L G Q R A T I S C R A S E S V D S Y G N G F I H W 40 Y Q Q K P G Q P P K L L I Y I L A S N I E S G V P A R F S G S S R T D F T L T I 80 D P M E A D D A A T Y Y C Q Q N N E D P R T F G G G T K L E I K R A </pre>	<p><b>Heavy Chain (VH)</b></p> <pre> 1 Q V Q L I K E S G G P G I V A P S Q S L S I T C T V S G F S L T D Y N I N W I R Q 40 P P G K G L E W L G M I W G D G S T A Y N S A L K S R L S I S K D N S S Q I F 80 82ab c 83 90 95 100 b c d e f 101 110 L K M N S L Q T E D T A R Y Y C A R D G Y F P Y A M A Y W G Q G T </pre>
118 S V T V S S	(SEQ ID NO 6)

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

**FIGURE 10**  
**227-26 Antibody**  
**Heavy Chain (VH)**

## Light Chain (VK)

1	10	20	30
	D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q S I V H S N G N T Y L Q		
40	50	60	70
	W Y L Q K P G Q S S P K L L I Y K V S N R F S G V P D R F S G S G S G T D F T L		
80	90	100	114
	I S R V E A E D L G V Y Y C F Q G S H V P Y T F G G G T K L E I K R A		(S E)

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 11 A

VK CHAIN

FM1

SEQ ID NO

FR2

SEQ ID  
NO

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	CDR1	49	41	42	43	44	45	46	47	48	49	50	51	52	53	54	CDR2
Murine 22B1C-1	N	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	Q	R	A	T	I	S	C	20	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y	29	
Human Femailate	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	21	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone B	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	22	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone J	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	23	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone L	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	24	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone N	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	25	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone P	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	26	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
Clone R	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	27	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #1	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	28	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #9	D	I	V	M	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	29	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #14	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	30	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #17	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	31	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #21	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	32	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #26	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	33	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #45	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	34	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #57	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	35	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #70	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	36	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #73	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	37	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #74	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	38	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #78	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	39	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #79	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	40	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #80	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	41	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #87	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	42	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #75	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	43	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #84	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	44	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #91	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	45	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #90	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	46	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #602	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	O	47	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #522	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	O	48	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #111	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	49	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #145	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	50	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #16	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	51	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #17	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	52	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #43	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	53	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #622	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	54	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #139	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	55	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #77	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	56	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		
HT2-NEW #313	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	57	W	Y	Q	Q	K	P	G	Q	P	P	K	L	I	Y		

FIGURE 11C

**FIGURE 11 B**

**FIGURE 11 D**

FIGURE 12A

VH CHAIN	SEQ ID NO	FR2		SEQ ID NO	FR2
		FR1	FR2		
Murine 2885C	1 2 3 4 5 6 7 8 9 0 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 CDR1 36 37 38 39 40 41 42 43 44 45 46 47 48 49 CDR2	QVQLQEESGPGLVAPQSLSITCTIVSIGFSLLN	WV R Q P P G K G L E W L G 67		
DP27		QVTLRESGPVALVKPTQTLSITCTIVSGFSLLS	W I R Q P P G K G L E W L A 68		
NEW		QVQQLQEESGPGLVRPSQTLSITCTIVSGFSLLS	W V R Q P P G K G L E W L G 69		
Clone 1		QVTLRESGPVALVKPTQTLSITCTIVSGFSLLN	W V R Q P P G K G L E W L G 70		
Clone 2		QVTLRESGPVALVKPTQTLSITCTIVSGFSLLS	W I R Q P P G K G L E W L A 71		
Clone 3		QVTLRESGPVALVKPTQTLSITCTIVSGFSLLS	W V R Q P P G K G L E W L G 71		
Clone 4		QVTLRESGPVALVKPTQTLSITCTIVSGFSLLN	W V R Q P P G K G L E W L G 71		
Clone 5		QVQQLQEESGPGLVYRPSQTLSITCTIVSGFSLLN	W V R Q P P G K G L E W L G 71		
H12-NEW#4		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#9		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#14		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#17		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#21		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#36		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#45		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#57		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#70		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#73		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#74		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#78		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#79		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#80		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#87		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#1275		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#4264		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#291		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#320		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#322		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#322		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#11		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#45		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#16		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#17		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#45		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#62		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#39		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#77		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		
H12-NEW#43		QVQLQEESGPGLVYRPSQTLSITCTIVSGSSTFS	W V R Q P P G K G L E W L G 71		

**FIGURE 12C**

EM1

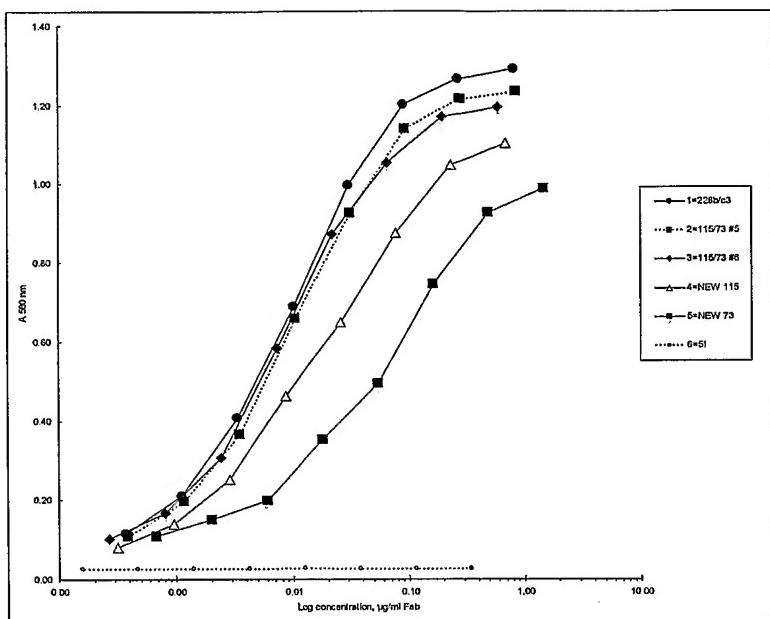
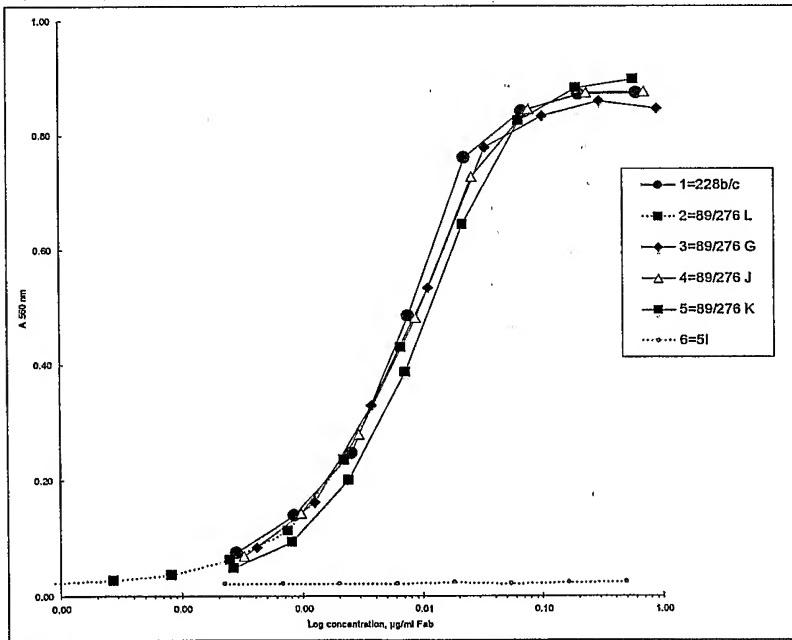
FIGURE 12B

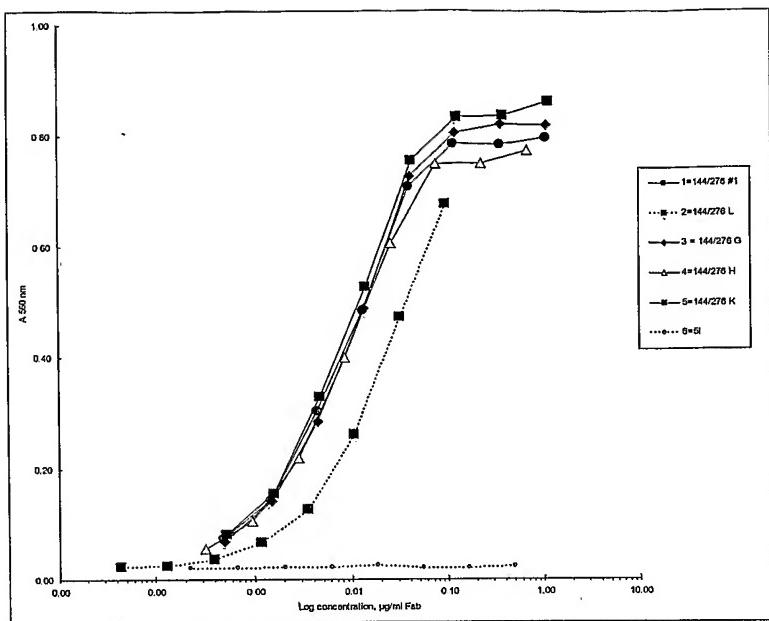
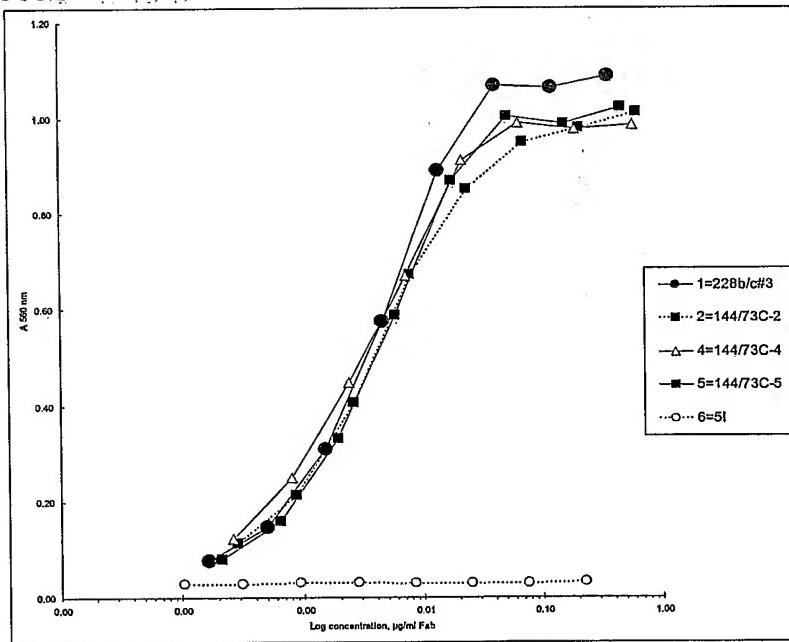
SEQ ID NO	FR4											
	66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 82A 82C 83 84 85 86 87 88 89 90 91 92 93 94 CD83 103 104 105 106 107 108 109 110 111 112 113											
R L N I S K D S S K S Q V F L K M S S L Q S D D T A R Y Y C A G	76	W	G	H	G	T	S	V	T	V	S	S
R L T I S K D T S S K N Q V F L T M S S V T A A D D T A V Y Y C A R	77	W	G	Q	G	S	L	V	T	V	S	S
R V T M L K D T S K N Q F S L R L S S V T A A D D T A V Y Y C A R	78	W	G	Q	G	S	L	V	T	V	S	S
R L T I S K D S S K N Q V F L T M T N M D P V D D T A T Y Y C A G	79	W	G	H	G	S	L	V	T	V	S	S
R L T I S K D S S K N Q V F L T M T N M D P V D D T A T Y Y C A G	80	W	G	H	G	S	L	V	T	V	S	S
R L T I S K D T S S K N Q V F L T M T N M D P V D D T A R Y Y C A G	81	W	G	Q	G	S	L	V	T	V	S	S
R L T I S K D T S K N Q V F L T M T N M D P V D D T A R Y Y C A G	82	W	G	Q	G	S	L	V	T	V	S	S
R L N M S K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	83	W	G	Q	G	S	L	V	T	V	S	S
R V N W S K D T S K N Q F F L R L S S V T A A D D T A V Y Y C A R	84	W	G	Q	G	S	L	V	T	V	S	S
R L N M S K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	85	W	G	Q	G	S	L	V	T	V	S	S
R L N W S K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	86	W	G	Q	G	S	L	V	T	V	S	S
R L N W S K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	87	W	G	Q	G	S	L	V	T	V	S	S
R V N M S K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	88	W	G	Q	G	S	L	V	T	V	S	S
R V N M S K D T S K N Q F F L R L S S V T A A D D T A V Y Y C A R	89	W	G	Q	G	S	L	V	T	V	S	S
R V T M L K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	90	W	G	Q	G	S	L	V	T	V	S	S
R V T M L K D T S K N Q F F L R L S S V T A A D D T A V Y Y C A R	91	W	G	Q	G	S	L	V	T	V	S	S
R V T M L K D T S K N Q F F L R L S S V T A A D D T A R Y Y C A G	92	W	G	Q	G	S	L	V	T	V	S	S

FIGURE 12D

三

SEQ ID NO

**FIGURE 13 A****FIGURE 13 B**

**FIGURE 13 C****FIGURE 13 D**

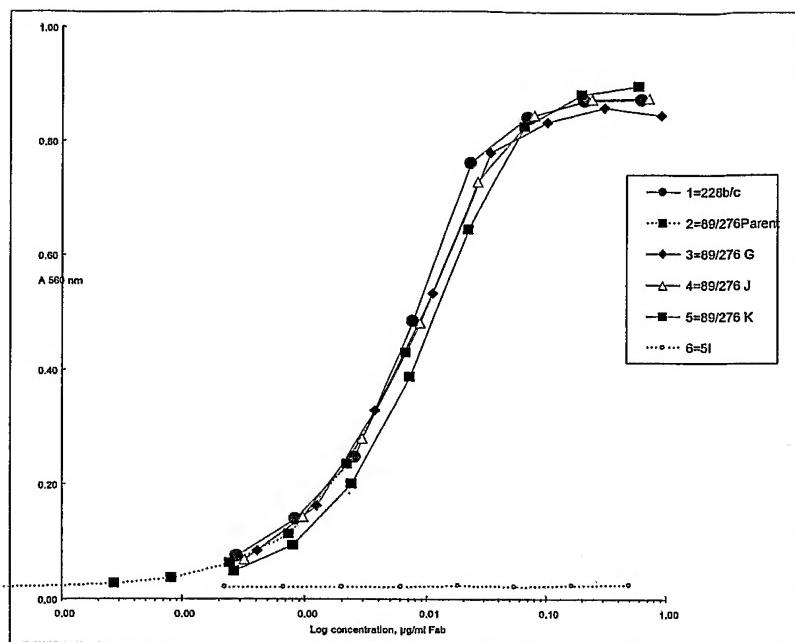
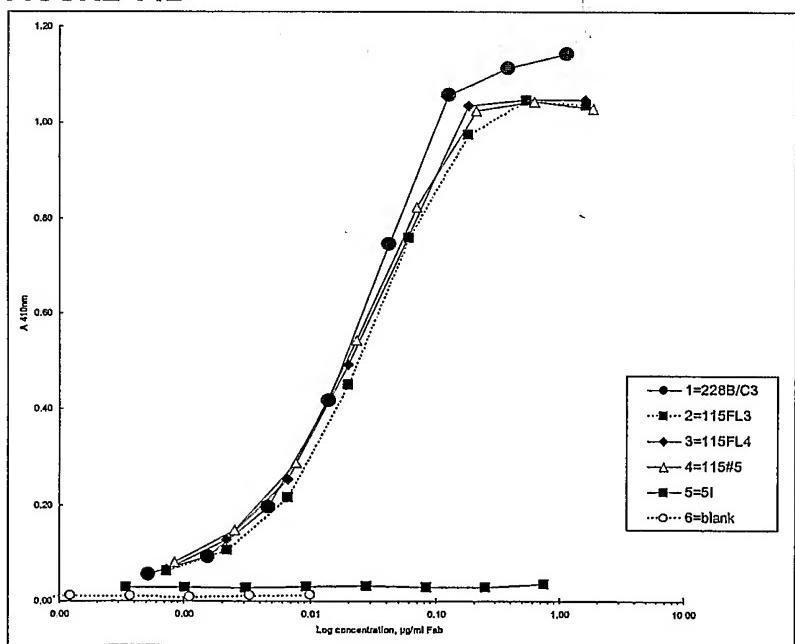
**FIGURE 14 A****FIGURE 14B**

FIGURE 15

L1-59 (parent)	CDR-L1	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H		
CL-5	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-13	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-42	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-48	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-50	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-56	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-65	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-69	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-82	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
CL-94	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H			
L1-59 (parent)	CDR-L3	Q	Q	N	N	E	D	P	R	T								
CL-5	Q	Q	N	A	E	D	P	R	T									
CL-13	Q	Q	N	N	E	D	P	R	T									
CL-42	Q	Q	N	A	E	D	P	R	T									
CL-48	Q	Q	N	N	E	D	P	R	T									
CL-50	Q	Q	N	A	E	D	P	R	T									
CL-56	Q	Q	N	A	E	D	P	R	T									
CL-65	Q	Q	N	N	E	D	P	R	T									
CL-69	Q	Q	N	A	E	D	P	R	T									
CL-82	Q	Q	N	N	E	D	P	R	T									
CL-94	Q	Q	N	A	E	D	P	R	T									
L1-59 (parent)	CDR-H1	A	Y	S	V	N												
CL-5	A	Y	S	V	N													
CL-13	A	K	S	V	N													
CL-42	A	N	S	V	N													
CL-48	A	N	S	V	N													
CL-50	A	K	S	V	N													
CL-56	A	K	S	V	N													
CL-65	A	S	S	V	N													
CL-69	A	N	S	V	N													
CL-82	A	N	S	V	N													
CL-94	A	N	S	V	N													
L1-59 (parent)	CDR-H3	D	G	Y	Y	P	Y	A	M	D	N							
CL-5	D	G	Y	Y	P	Y	A	M	K	N								
CL-13	D	G	Y	Y	P	Y	A	M	S	N								
CL-42	D	G	Y	Y	P	Y	A	M	K	N								
CL-48	D	G	Y	Y	P	Y	A	M	K	N								
CL-50	D	G	Y	Y	P	Y	A	M	K	N								
CL-56	D	G	Y	Y	P	Y	A	M	S	N								
CL-65	D	G	R	Y	P	Y	A	M	K	N								
CL-69	D	G	Y	Y	P	Y	A	M	D	N								
CL-82	D	G	Y	Y	P	Y	A	M	K	N								
CL-94	D	G	Y	Y	P	Y	A	M	K	N								

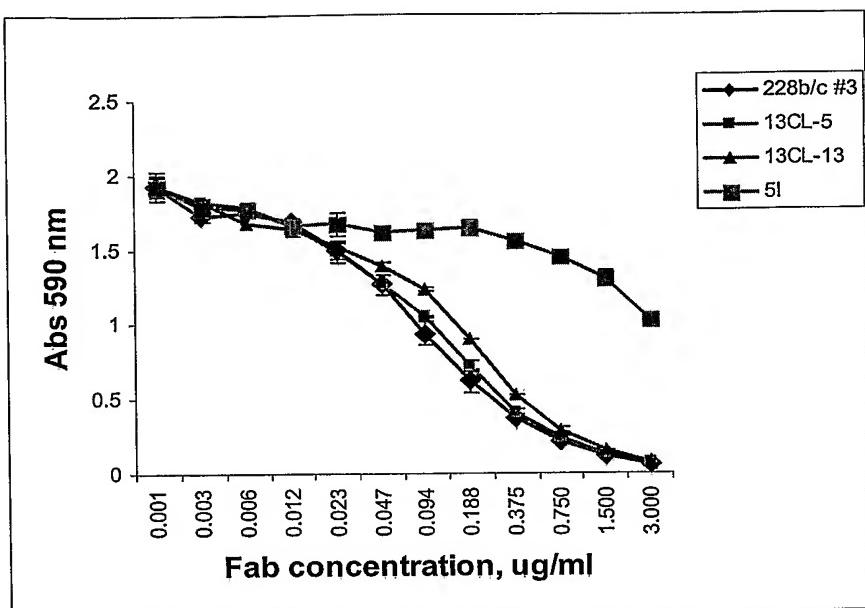
**FIGURE 16**

Figure 17 Variable Region Amino Acid Sequences for anti-II.13 Candidates

CL-5 (Affinity Matured Candidate) V<sub>k</sub>:

DIVMTQSPDSLSSVLGERATINCRASKSYGQOSFMHWYQQKPGQPPKLLIYLASNLESGVPDFSGSGSGTDFLT  
 LTISSLQAEDEVYYCQQNAEDPRTFGGGTKVEIKR (SEQ ID NO 93)

CL-5 (Affinity Matured Candidate) V<sub>h</sub>:

QVTLRESGPALVKPTQTLTCTGSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN  
 QVVLTMNTNMDPVVDATYYCAVDGYYPPYAMKNNWGGQSLSLVTVSS (SEQ ID NO 94)

CL-13 (Affinity Matured Candidate) V<sub>k</sub>:

DIVMTQSPDSLSSVLGERATINCRASKSYGQOSFMHWYQQKPGQPPKLLIYLASNLESGVPDFSGSGSGTDFLT  
 LTISSLQAEDEVYYCQQNNEDPRTFGGGTKVEIKR (SEQ ID NO 95)

CL-13 (Affinity Matured Candidate) V<sub>h</sub>:

QVTLRESGPALVKPTQTLTCTGSGFSLSAKSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN  
 QVVLTMNTNMDPVVDATYYCAVDGYYPPYAMSNWGGQSLSLVTVSS (SEQ ID NO 96)

CL-50 (Affinity Matured Candidate) V<sub>k</sub>:

DIVMTQSPDSLSSVLGERATINCRASKSYGQOSFMHWYQQKPGQPPKLLIYLASNLESGVPDFSGSGSGTDFLT  
 LTISSLQAEDEVYYCQQNAEDPRTFGGGTKVEIKR (SEQ ID NO 97)

CL-50 (Affinity Matured Candidate) V<sub>h</sub>:

QVTLRESGPALVKPTQTLTCTGSGFSLSAKSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN  
 QVVLTMNTNMDPVVDATYYCAVDGYYPPYAMKNNWGGQSLSLVTVSS (SEQ ID NO 98)

FIGURE 18

## Alignment of IL13 protein sequences

Majority

M A L W L T A V I A L A C L G G U A S P G P V P	- - - P S T A L K E L I E E L
1 M A L W L T T V I A L T C L G G F A S P G P V P	- - - P S T A L K E L I E E L
1 M A L W L T M V I A L T C L G G F A S P S P V P	- - - P S T A L K E L I E E L
1 M A L W L T A V I A L T C L G G F A S P S P V P	- - - S A T A L K E L I E E L
1 M A L W L T A V I A L T C L G G F A S P S P V P	- - - S A T A L K E L I E E L
1 M A L W L T V V I A L T C L G G L A S P S P V P	- - - P S P T A L K E L I E E L
1 M A L W L T V V I A L T C L G G L A S P S P V P	- - - P S P T A L K E L I E E L
1 M A L W V T A V I A L A C L G G L A T P G P V	- - - P V A L E L I E E L
1 M A L W V T A V I A L A C L G G L A A P G P V	- - - P V A L E L I E E L
1 M A L W L T A V I A L A C L G G L A S P V S P	- - - P V A L E L I E E L
1 M A L W L T A V I A L A C L G G L A V D G P V	- - - P V A L E L I E E L
V N I T Q N Q K A P L C N G S M V W S V N L T A G Y C A A L E S L I N I S G C	Majority
37 V N I T Q N Q K A P L C N G S M V W S V N L T A G Y C A A L E S L I N I S G C	Human.pro
37 V N I T Q N Q K V P L C N G S M V W S V N L T A G Y C A A L E S L I N I S G C	Monkey-cyn
37 V N I T Q N Q K V P L C N G S M V W S V N L T A G Y C A A L D S L I N I S N C	Bovine.pro
37 V N I T Q N Q - A S I L C N G S M V W S V N L T A G Y C A A L E S L I N I S D C	Dog.pro
41 S N I T Q D O - T P L C N G S M V W S V D L I T A G G F C A A L E S L I T N I S S C	Rat.pro
41 S N I T Q D O - T P L C N G S M V W S V D L I A A C G G F C V A L D S L I T N I S N C	Mouse.pro
41 S N I T Q D O - T P L C N G S M V W S V D L I A A C G G F C V A L D S L I T N I S S C	Gerbil.pro
S A I Q R T Q R M I N G L C P H K A S A G Q - S S S R V R D T K I E V A Q F V K	Majority
77 S A I E K T Q R M I S G F C P H K V S A G Q F S S I L H V R D T K I E V A Q F V K	Human.pro
77 S A I E K T Q R M I N G E C P H K V S A G Q F S S I L R V R D T K I E V A Q F V K	Monkey-cyn
77 S V I Q R T K K M I N A L C P H K P S A K O V S S E V V R D T K I E V A Q F L I K	Bovine.pro
76 S A I Q R T Q R M I K A L C I S Q P A G Q I S S E R S E R D T K I E V A Q F L I K	Dog.pro
81 N A I Y R T Q R I T I N G L C N R K A S D - - V A S S P D T K I E V A Q F I S	Rat.pro
80 N A I Y R T Q R I T I H G L C N R K A P T - - T V S S L P D T K I E V A H F I T	Mouse.pro
81 N T I Q R T Q R I T I N G L C A R K A P A - - V V S R V P D T K I E V A Q F I K	Gerbil.pro
D L N N Y S K U L F R N G K F N	Majority
117 D L L H L K K L F R E G R F N	
117 D L L V H L K K L F R N G R F N	
117 D L L R H S R I V F R N E R F N	
116 N L L T V R G V Y P R H G N E R	
118 K I L N Y S K O L F R Y G H	
117 K L L S V T K Q L F R H G P E	
118 N L L N Y S K Q	

Figure 19 IL13 and the Binding Epitope of 228B/C MAb

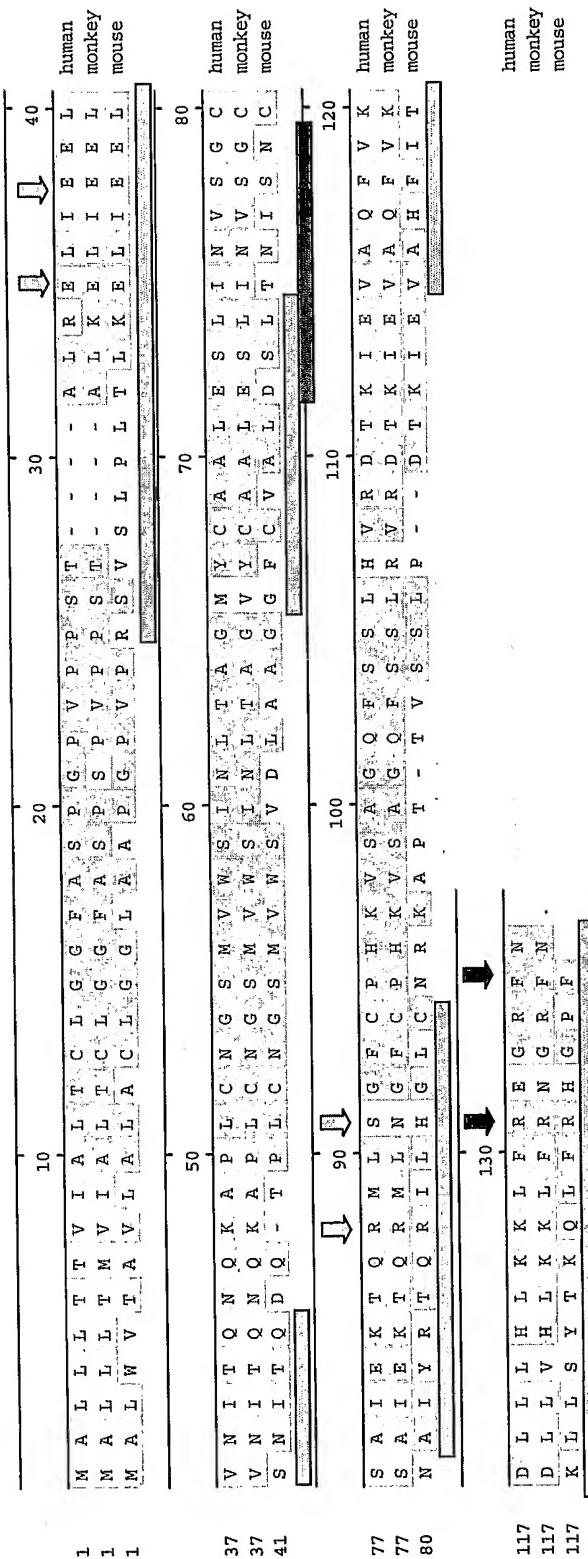


FIGURE 20

<b>CDR-L1</b>		<b>CDR-H1</b>			
P	RASKSVDSYGNNSFMH	SEQ ID NO 99	P	AYSVN	SEQ ID NO 117
V1	RASKSVDSYGQSFMH	SEQ ID NO 100	V1	AKSVN	SEQ ID NO 118
V2	RASKSVDSYQGSFLH	SEQ ID NO 101	V2	ANSVN	SEQ ID NO 119
V3	RASKSVDSYGNNSYMH	SEQ ID NO 102	V3	GYSVN	SEQ ID NO 120
V4	RASKSVDSYGNFLH	SEQ ID NO 103	V4	AHSVN	SEQ ID NO 121
			V5	ARSVN	SEQ ID NO 122
<b>CDR-L2</b>		<b>CDR-H2</b>			
P	LASNLES	SEQ ID NO 104	P	MIWGDGKIVVNSALKS	SEQ ID NO 123
V1	LASNLLNS	SEQ ID NO 105	V1	MIWGDGKISVNSALKS	SEQ ID NO 124
V2	LASNLQS	SEQ ID NO 106	V2	MIWGDGKIVVNSALES	SEQ ID NO 125
V3	LATNLES	SEQ ID NO 107	V3	MIWGDGKIVVNSALKS	SEQ ID NO 126
V4	LASNLKs	SEQ ID NO 108	V4	MIWGDGKIVVNSDLKS	SEQ ID NO 127
V5	LASNLEK	SEQ ID NO 109	V5	MIWGDGKIVVNSALKS	SEQ ID NO 128
V6	LASRLES	SEQ ID NO 110	V6	MIWGDGKIVVNSELKS	SEQ ID NO 129
V7	LASNLLHS	SEQ ID NO 111	V7	MIWGDGKIAVNSALKS	SEQ ID NO 130
V8	LASNLLSS	SEQ ID NO 112	V8	MIWGDGKIVVNSALKE	SEQ ID NO 131
V9	LASFLES	SEQ ID NO 113	V9	MVWDGKIVVNSALKS	SEQ ID NO 132
V10	LANNLES	SEQ ID NO 114	V10	MIWGDGKIVVNSALAS	SEQ ID NO 133
			V11	MIWGDGKKVNSALKS	SEQ ID NO 134
<b>CDR-L3</b>		<b>CDR-H3</b>			
P	QQNNEDPRT	SEQ ID NO 115	P	DGYYPYAMDN	SEQ ID NO 135
V1	QQNAEDPRT	SEQ ID NO 116	V1	DGRYPYAMDN	SEQ ID NO 136
			V2	DGYYPYAMKN	SEQ ID NO 137
			V3	DGRYPYAMKN	SEQ ID NO 138
			V4	DGYYPYAMSN	SEQ ID NO 139
			V5	DGYYPYAMAN	SEQ ID NO 140
			V6	DGYYPYALDN	SEQ ID NO 141

FIGURE 21A: Variable Region Amino Acid Sequences for certain anti-IL 13 Candidates:CL-89 V<sub>k</sub> (SEQ ID NO: 142):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWYQQKPPKLLIYLASNLESGVPDRFSSGGT  
 DFTLTISLQAEDDVAVYCCQNNEDPRTFGGGTKVEIKR

CL-276G V<sub>h</sub> (SEQ ID NO 143):

QVTLRESGPALVKPTQTTLTCTVGFFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDT  
 KNQVVVLTMNTNMDPVDTATYYCAGDGYYPYAMDNWGQGSLVTVSS

RL-36 (Random Library Candidate) V<sub>k</sub> (SEQ ID NO 144):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWYQQKPPKLLIYLASNLESGVPDRFSSGGT  
 DFTLTISLQAEDDVAVYCCQNNEDPRTFGGGTKVEIKR

RL-36 (Random Library Candidate) V<sub>h</sub> (SEQ ID NO 145):

QVTLRESGPALVKPTQTTLTCTGSGFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDT  
 KNQVVVLTMNTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLVTV  
 SS

RL-19 (Random Library Candidate) V<sub>h</sub> (SEQ ID NO 146):

QVTLRESGPALVKPTQTTLTCTSSGFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDT  
 KNQVVVLTMNTNMDPVDTATYYCALDGYYPYAMDNWGQGSLVTV  
 SS

29/29

**FIGURE 21B:** Variable Region Amino Acid Sequences for certain anti-IL13 Candidates:  
RL-11 (Random Library Candidate) Vh (SEQ ID NO 147);

QVTLRESGPALVKPTQTLTCTSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS  
KNQVVLTMTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLVT  
SS

RL-8 (Random Library Candidate) Vh (SEQ ID NO 148):

QVTLRESGPALVKPTQTLTCTLSGFSLSAYSVNWIRQPPGKALEWLAMINWGDGKIVYNSALKSRLTISKDTSS  
NQVVLTMTNMDPVDTATYYCASDGYYPYAMMDNWGQGSLVTV  
SS

RL-45 (Random Library Candidate) Vh(SEQ ID NO 149):

QVTLRESGPALVKPTQTTLTCTSGFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS  
KNQVVLTMTNMDPVDTATYYCATDGYYPYAMDNWGQGSLVTV  
SS

RL36-L1.59 (L1 Affinity Matured Candidate) V/k (SEQ ID NO 150):

DIVMTQSPDLSVSLGERATINCRAKSVDSYQQSFMHWYQQKPGQPPPKLILYLASNLESGVPDRFSGSGSGT  
DFTLTSSQLQAEDVAVYQQNNEDPRTFGGGTKVEIKR

RL36-L1,59 (L1 Affinity Matured Candidate) Vh (SEQ ID NO 151):  
QVTLLRESGPALVKPTQTLLTCTGSGFSLSAYSVNNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS  
KNQVVVLTMNTMDPVDTATYYCAVDGYYPYAMDNWGQQGLVTSS

scEVY Candidate #212 (SEQ ID NO 1152):